

Analysis of diversity in wild and cultivated common beans from Argentina

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Northwestern Argentina is the southernmost limit of the Andean domestication area of common bean hosting, like other areas in South America, wild relatives of beans, which are the main source of variability of beans. In addition, different cultivars developed at CIAT that are adapted to the environmental conditions of the country have been introduced and incidentally turn out to be important commercial cultivars.

Argentina is a major producer and ranked third among countries exporting common beans. Therefore the genetic characterization of commercial cultivars and of wild relatives of common bean by molecular markers is particularly important to link markers to genetic traits of interest. Therefore the purpose of our work was to characterize and identify sources of bean diversity by means of molecular markers in commercial and wild cultivars.

The ten most important commercial cultivars of common beans were characterized based on RAPD and ISSR markers (Table 1). Out of 16 RAPD primers, 4 showed polymorphisms among beans. Furthermore, cluster analysis and principal coordinates analysis associated beans either as members of the Andean or the Mesoamerican gene pool. These results were later confirmed by means of ISSR, which turn out to be better tools than RAPD markers to identify beans by their gene pool of origin though not to show differences between individuals.

Burkart and Bruchner (1953) describe the existence of wild populations of beans in the provinces of Jujuy, Salta, Tucuman, San Luis and Córdoba. Because these places have different environmental conditions and are geographically distant the development of landraces and wild populations might have been favored suggesting the existence of either genomic plasticity or genetically diverse beans. Therefore, we analyzed diversity of 10 wild populations of common bean based on morphological and molecular markers such as RAPD and ISSR. Even though molecular markers unlike morphoagronomic traits are neutral, they grouped bean populations, same as agronomic traits, based on their site of collection. The dendrogram showed low levels of diversity suggesting also a common ancestor. Partitioning of the genetic variation between wild populations and agroecological areas by molecular markers (RAPD and ISSR) indicated that a considerable part of it was attributable to differences within populations. These results showed a less geographical structure of the Andean wild beans compared to the Mesoamerican ones.

Table 1. RAPD and ISSR polymorphic primer sequences used for analysis of ten cultivars of *Phaseolus vulgaris* L. with primer annealing temperatures and number of polymorphic bands amplified.

Primer name	Primer sequence (5'-3')	Annealing temp. (°C)	Number of polymorphic bands
RAPD			
OPA 02	TGCCGAGCTG	36	3
OPA 09	GGGTAACGCC	36	4
OPA 20	GTTGCGATCC	36	6
OPE 20	AACGGTGACC	36	4
ISSR			
1	GAG(CAA) ₅	52	5
4	CTC(GT) ₈	54	3
6	(AG) ₈ CG	54	2
7	(AG) ₈ TG	52	5
11	(AG) ₈	49	2
13	(CCA) ₅	55	4
16	(AC) ₈	57	5
19	(GCC) ₅	66	5
23	(GAA) ₅	54	2

Reference

Burkart A, Brücher H. 1953. *Phaseolus aborigineus* Burkart, die mutmaßliche andine Stammform der Kulturbohne. Der Züchter 23:65-72.

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